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FOREWORD

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A: INTRODUCTION

Human oncostatin M (OM), a product of activated T cells and macrophages, is a 28 kDa glycoprotein that regulates cell growth and differentiation. OM stimulates the growth of normal fibroblasts, normal vascular smooth muscle cells, and myeloma cells. OM also has been shown to inhibit the proliferation of a number of cell lines derived from human tumors including melanoma and lung carcinoma (1-7). The growth inhibitory or growth stimulatory activity exhibited by OM seems to depend on target cell type.

OM signal transduction occurs through two types of heterodimeric receptors (8-10). A shared receptor mediates both OM, LIF and CT-1 signals and is composed of the LIF receptor α subunit and gp130 (9,11). Many overlapping functions of OM and LIF are mediated through this common receptor. However, we and others have demonstrated that a specific OM receptor exists in certain cell types including breast cancer cells. (9,10,12). Therefore, In the grant, we originally proposed to isolate and characterize this OM specific receptor and we predicted that the OM-specific receptor transduces exclusively OM signals and would be consist of gp130 as a binding subunit and a second subunit as an affinity conversion subunit. However, during our initial work to construct a cDNA library and to clone this second subunit, an abstract reporting the isolation of signaling subunit of OM receptor was published in the full of 1994 at the International Cytokine Society Meeting. Bruce Mosley at Immunex reported the cloning of this subunit (13). Therefore, we decided not to waste our resource to continue to clone this subunit, instead to start a collaboration with Immunex to characterize the expression of this newly identified molecule in breast cancer and in normal mammary epithelial cells, and to investigate the functional roles of OM-specific receptor versus the OM/LIF shared receptor in OM mediated growth inhibition, since currently, little is known about how the cellular growth response to OM is controlled at the receptor level, and the molecular mechanism(s) by which OM regulates cell growth remains largely uncharacterized. Unfortunately, although Immunex had agreed to provide the cDNA of OSMR β for our transfection experiment in the beginning of 1995, their manuscript that describes the cDNA sequence and cloning procedure was delayed for publication until December 1996 (14). Therefore, we were unable to start the experiments as planed in our grant. Recently, we have establised the material transfer agreement for the OSMR β cDNA (April 7, 1997, see attached). As oon as the cDNA becomes avaiable, we will begin to perform the transfection experiments.

In the mean time, we have continued our study to examine the biological functions of OM in breast cancer cells. Previously, we have examined the effects of OM on 10 breast cancer cell lines and on normal human mammary epithelial (HME) cells derived from 4 donors. Our data showed that the cellular proliferation of 7 out of the 10 breast cancer cell lines was inhibited by OM. The 3 cell lines that did not respond to OM treatment lacked OM high affinity binding sites. The growth inhibitory activity of OM is partially due to its functional antagonism of breast cancer mitogens including EGF, EGF-like growth factor, and bFGF and also to its effect on transcriptional suppression of the c-myc protooncogene. In contrast to the selective effect of OM on breast cancer cells, all of the HME cells examined were growth-inhibited by OM. These results led us to examine and to compare the expression levels of the two OM receptors, the OM-specific receptor composed of gp130 and OSMR β and the OM/LIF shared receptor (LIFR), in HME and breast cancer cells. The flow cytometry analysis utilizing anti-gp130 and anti-OSMR β

showed that the expression levels of the OM-specific receptor are much higher in HME cells than in breast cancer cells. The OM-nonresponsive breast cancer cells express gp130, the ligand binding subunit, but the OSMR β , the signaling subunit is undetectable. This suggests that the expression of the signaling component of the OM-specific receptor is dysregulated in breast cancer cells, and this may account for the loss of responsiveness to OM. Compared with the OM-specific receptor, the expression of the OM/LIF shared receptor is lower in both HME and breast cancer cells. Interestingly, neither the HME cells nor the breast cancer cells were growth-inhibited by LIF. In fact, LIF slightly stimulated the proliferation of breast cancer cells. These data suggest that OM and LIF have different effects on mammary epithelial cells and that the effects of OM are mediated by the OM-specific receptor. Taken together, these studies suggest that OM may function as a negative growth regulator for mammary epithelial cells through the interaction with the OM-specific receptor. The decreased or lost expression of this receptor, particularly the signaling subunit (OSMR β), would result in an imbalance of the growth-stimulatory and growth-inhibitory regulation exerted in the microenvironment of breast tissue. This may be one of the factors contributing to the development of breast tumors.

To extend these studies and to establish the possible roles of OM in human breast malignancy, we have focused our investigations into three different aspects. 1. to examine the effect of OM on the expression of breast cancer specific genes which play critical roles in tumor promotion, 2. to examine the signaling transduction pathways that lead to inhibition of tumor cell growth, and 3. to examine the role of endogenous OM, produced by the host defense system (T cells and macrophages) in breast cancer development by immunohistochemistry.

In this report, we show that: (1) The breast cancer specific gene 1 (BCSG1) is highly expressed in infiltrating breast carcinoma but not expressed in normal breast tissue. (2) The expression of BCSG1 is transcriptionally suppressed by OM. (3). The antagonism of OM to EGF mitogenic activity is mediated in part by inhibiting EGF-induced cellular tyrosine phosphorylation event. (4) Detection of OM in tissue samples of breast carcinoma and ovarian carcinoma.

B. MATERIALS AND METHODS

Cells and Reagents. The human breast cancer cell line H3922 was developed from a ductal infiltrating breast carcinoma at the Bristol-Myers Squibb Pharmaceutical Research Institute-Seattle. The cells were cultured in Iscoves Modified Dulbecco's Medium (IMDM) supplemented with 10% heat-inactivated fetal bovine serum (FBS). Human recombinant OM was expressed by Chinese hamster ovary cells and purified as previously described (22). The other growth factors and cytokines were obtained from R&D Systems, Minneapolis, MN. The plasmid containing the cDNA probe for *c-Myc* was obtained from ATCC. A human glyceraldehyde-3-phosphate dehydrogenase (*GAPDH*) cDNA probe was generously provided by Dr. Jeff L. Ellsworth at CV Therapeutics, Palo Alto, CA.

Northern Blot Analysis

Total cellular RNA was isolated by the method of Poppel and Baglioni. Approximately 20 μ g of each total RNA sample was separated on a 1.0% formaldehyde agarose gel. RNA was capillary transferred to a Hybond N membrane before crosslinking to the membrane. Prehybridization and hybridization steps were performed under the conditions previously described. The blot was hybridized at 60° C to a 0.55 Kb 32 P-labeled human *BCSG1* cDNA probe. The probe was labeled using 50 μ Ci [α - 32 P] dCTP with random primed DNA labeling kit (Boehringer Mannheim Corp, Indianapolis, IN). The membrane was then washed 3 times at ambient temperature with 2X SSC, 0.1% SDS and twice at 37° C with 0.1X SSC, 0.1% SDS. The membrane was then dried and exposed to X-OMAT scientific imaging film (Kodak, Rochester, NY) for 1-3 days at -80° C. The *c-Myc* and *GAPDH* probes were prepared by random-primer labeling as described for the *BCSG1* probe. All other steps in analysis of the membrane were also followed as described for the *BCSG1* probe. The autoradiographs were scanned by a laser densitometer (Personal DensitometerTM SI, Molecular Dynamics, Sunnyvale, CA) and the integrated intensity of each band was analyzed with the program ImageQuaNTTM, version 4.1. Densitometric analysis of autoradiographs in these studies as well as those discussed below included various exposure times to ensure linearity of signals.

Nuclear Run-on Analysis. These analyses were conducted using a procedure adapted from one that had already been described. Briefly, 1.8×10^7 adherent H3922 cells were harvested with cell scrapers into a minimal volume of cold phosphate buffered saline (PBS). The cells were pelleted by low-speed centrifugation and lysed with lysis buffer (10 mM Tris-HCl, pH 7.9, 10 mM NaCl, 3 mM MgCl₂, 0.5% Nonidet P-40). The nuclei were pelleted by centrifugation and the lysis procedure was repeated once. The nuclei were recovered by centrifugation a second time and resuspended at 10^8 nuclei/ml in glycerol storage buffer (50 mM Tris-HCl, pH 8.3, 40% glycerol, 5 mM MgCl₂, 0.1 mM EDTA). The nuclei samples were immediately frozen under liquid nitrogen and stored at -80° C.

The frozen nuclei were subsequently thawed and 100 μ l of each sample received 100 μ l 2X reaction buffer (70% glycerol, 0.02 M Tris-HCl, pH 7.5, 0.01 M MgCl₂, 0.16 M KCl, 2 mM DTT, 0.2 mM EDTA, 2 mM rATP, 2 mM rCTP, 2 mM rGTP, 2.6 μ Ci/ μ l [32 P] rUTP). The reactions were incubated, with shaking at 30° C for 30 minutes. Labeled nuclei were

pelleted and resuspended with 100 μ l DNase buffer (50% glycerol, 20 mM Tris-HCl, pH 7.9, 1 mM MgCl₂, 10 mg/ml RNase-free DNase I). The reactions were incubated with shaking at 30°C for 15 minutes. Samples were brought up to 125 μ l with 7.5 μ l 13.6 mg/ml proteinase K, 5 μ l 10 mg/ml yeast tRNA, and 12.5 μ l 10X SET buffer (5% SDS, 0.05 M EDTA, 0.01 M Tris-HCl, pH 7.4) and incubated at 42°C for 30 minutes.

Labeled RNA transcripts were extracted by adding the following: 275 μ l GCSM solution [4 M guanidinium isothiocyanate, 0.025 M sodium citrate, pH 7.0, 0.5% Sarkosyl, 0.1 M β -mercaptoethanol], 45 μ l 2.0 M sodium acetate, 450 μ l water-saturated phenol, and 90 μ l chloroform:isoamyl alcohol (49:1). The samples were vortexed and incubated on ice for 15 minutes. Nuclear run-on transcripts were precipitated with isopropanol and pelleted by high speed centrifugation. Extractions and isopropanol precipitations were repeated and the samples were dissolved with 102 μ l TES buffer (10 mM Tris-HCl, pH 7.4, 1 mM EDTA, 0.1% SDS). Assays for radioactivity were conducted by liquid scintillation. Approximately 2.0×10^6 cpm of each nuclear run-on reaction was used as a probe to hybridize a Hybond N membrane (Amersham Life Sciences, Arlington Heights, IL) slot blot. Each blot received the following three plasmids: 5 μ g plasmid with the human *GAPDH* cDNA insert, 3 μ g of the 0.3 kb fragment of the *BCSG1* cDNA which is the 3' end of the cDNA. This fragment was generated by cutting the *BCSG1* cDNA with the restriction endonuclease BstX1. Probing the *GAPDH* plasmid allowed normalization of the *BCSG1* signals measured by densitometry.

Actinomycin D/mRNA Stability Analysis. H3922 cells in 100 mm tissue culture plates were incubated with or without OM for 6 h. Actinomycin D (5 μ g/ml) was added to cells for different lengths of time. At the end of each time point, total RNA was harvested as described above under "Northern Blot Analysis". Electrophoresis of total RNA samples, blotting, and hybridization to radiolabeled probes were also carried out as described above.

Cell Proliferation Assay

Cells were seeded in 96-well tissue culture plates (Costar, Cambridge, MA) in IMDM medium containing 2% FBS at a density of 3000 cells/well in 100 μ l of medium. Three to 5 hours after seeding, 50 μ l of the same culture media containing various factors was added to each well. Three days later [³H]thymidine (0.5 μ Ci/50 μ l/well) in medium was added to the culture plates 4 hours prior to harvest. The amount of [³H]thymidine incorporated into cells was measured using a liquid scintillation counter (Pharmacia, Piscataway, NJ). The differences in counts/min incorporated between experimental and control cultures were used as an index for DNA synthesis. Each data point represents the average of triplicate cultures and each experiment was performed at least 3 times.

Immunoprecipitation and Immunoblotting. H3922 cells were cultured in 60 mm culture plates for 2 days in 2% FBS IMDM with or without OM (100 ng/ml). The cells were then stimulated with 10 ng/ml of EGF for 10 minutes, or 100 ng/ml of OM for 15 minutes. Cells were rinsed with cold PBS and lysed with 0.5 ml of lysis buffer (50 mM Tris [pH 7.4], 1% NP-40, 0.25% sodium deoxycholate, 150 mM NaCl, 1 mM EGTA, 1 mM phenylmethylsulfonyl fluoride (PMSF), 1 mM Na₃VO₄, 1 mM NaF, 5 μ g/ml of aprotinin, 1 μ g/ml of leupeptin, and 1.25 μ g/ml of pepstatin). The cell lysate (250 μ l, approximately 1 μ g/ μ l of protein) was

precleared with 50 μ l of protein A-sepharose slurry and then incubated overnight with 30 μ l of sepharose-conjugated anti-phosphotyrosine monoclonal antibody 4G10. The sepharose beads were collected by microcentrifugation and resuspended in 50 μ l of 2X SDS sample buffer containing 5% β -mercaptoethanol. Immunoprecipitates were analyzed by western blot with anti-phosphotyrosine monoclonal antibody 4G10 using an enhanced chemiluminescence (ECL) detection system.

C. RESULTS

1. Transcriptional regulation of breast cancer specific gene (BCSG1) by oncostatin M

Northern blot analysis of BCSG1 expression in human breast cancer cell lines.

By utilizing a high-throughput direct-differential cDNA sequencing approach, a novel breast cancer specific gene, designated *BCSG1* was recently isolated from a breast tumor cDNA library (15). *BCSG1* gene is transcribed into a 1 kb mRNA, and the open reading frame of the full length gene is predicted to encode a 127-amino acid polypeptide. Comparison of the predicted amino acid sequence with genetic data base reveals that *BCSG1* is highly homologous to the non-A β fragment of human AD amyloid protein with 54% sequence identity (16).

BCSG1 mRNA expression was found exclusively in neoplastic epithelial cells. In situ hybridization analysis has demonstrated a stage-specific expression pattern of *BCSG1* mRNA varying from virtually no detectable expression in normal or benign breast tissue to low level and partial expression in low grade in situ breast carcinoma, to high expression in advanced infiltrating carcinomas. This implies that *BCSG1* may play a role in breast cancer malignant progression. The high level expression of BCSG1 in the neoplastic breast epithelial cells suggest that the expression of BCSG1 may be up-regulated in the mammary gland during breast cancer onset and progression.

Therefore, we initiate a study to examine BCSG1 expression in breast cancer cell lines. As shown in Figure 1, among the 8 different cell lines, BCSG1 mRNA was detected in 2/4 human breast cancer cell lines derived from pleural effusion and 4/4 breast cancer cell lines derived from ductal infiltrating carcinomas (ZR-75-1, MDA-MB-231, H3914, and H3922). In contrast, no hybridization signals were detected from mRNAs isolated from 4 normal breast tissues.

Dose- and time-dependence of OM-induced suppression of *BCSG1* mRNA expression in breast cancer cells.

Among the cell lines that were examined, H3922 expressed the highest level of *BCSG1* mRNA. Since OM has an inhibitory and differentiative effect on H3922 cell growth, we examined the effect of OM on *BCSG1* mRNA expression. The results in Figure 2 demonstrated a dramatic time-dependent suppression of *BCSG1* mRNA level by OM. Treatment of H3922 cells with OM initiated an immediate decrease of *BCSG1* mRNA as early as 30 minutes. By 4 h treatment, the level of *BCSG1* mRNA was decreased to 70% of that in control, and by 24 h, the mRNA was completely undetectable (Figure 2).

We next investigated the dose-dependent effect of OM on *BCSG1* gene expression. In order to be able to detect *BCSG1* mRNA in OM treated cells, H3922 cells were treated with OM for 6 h at different concentrations before the total RNA was harvested for northern blot analysis of *BCSG1* mRNA (Figure 3A). Densitometry analysis of *BCSG1* hybridization signal with normalization to *GADPH* signal (Figure 3B) showed that cells treated with 0.2, 1.0, 5.0, 25, and 125 ng/ml OM expressed 58%, 46%, 47%, 45%, and 41% as much *BCSG1* mRNA, respectively, as that observed in control cells treated with OM dilution buffer (1 mg/ml BSA in PBS). This data suggested that OM produced a maximum suppressive effect on *BCSG1* expression at a concentration of 1-5 ng/ml with an EC_{50} of 0.08 ng/ml. To compare the effective dose ranges of OM in its ability to elicit two different biological responses (cell growth and

BCSG1 gene expression), in parallel experiment, the OM-dose dependent effect on H3922 cell proliferation was also examined. As shown in Figure 3C, the maximal inhibitory effect of OM on H3922 DNA synthesis occurred at OM concentration of 20 ng/ml with an EC_{50} of 0.2-0.4 ng/ml.

Transcriptional regulation of *BCSG1* expression by oncostatin M.

To determine whether the down regulation of *BCSG1* expression by OM occurs at transcriptional or post-transcriptional levels, we conducted nuclear run-on assays to measure the relative transcription rate of *BCSG1* in control cells and in the cells treated with OM. As shown in Figure 4, upon the pretreatment with OM for 16 h, H3922 cells contained only 28.5% as many active *BCSG1* mRNA transcripts as that observed in control cells. Data were normalized by the signals observed in the *GADPH* slots. The level of reduction of BCSG1 transcripts is consistent with the results obtained from northern blot. These results suggest that transcriptional regulation is the major component of the observed OM-mediated suppression of *BCSG1* gene expression.

To further investigate the mechanisms by which OM inhibits the expression of the *BCSG1* gene in H3922 cells, *BCSG1* mRNA stability was examined. Control cells and the cells treated with OM for 6 h were exposed to actinomycin D. Total RNAs isolated from the cells at various actinomycin D exposure time points were subjected to northern blot analyses of *BCSG1*. (Figure 5). Although OM treatment reduced the level of *BCSG1* mRNA to approximately 50% of that in control cells, the *BCSG1* mRNA levels in both the control cells and the OM-treated cells were not decreased by actinomycin D. In contrast, the *c-Myc* mRNA levels were rapidly declined with the treatment of actinomycin D. These data suggest that the *BCSG1* mRNA stability was not altered by OM, and that the *BCSG1* mRNA is relatively stable. An attempt to treat cells with actinomycin D for a longer period of time was not successful due to the actinomycin D-mediated toxicity in H3922 cells. These results together with the data generated from the nuclear run-on assay suggest that the *BCSG1* gene expression was suppressed by OM at the transcriptional level.

***BCSG1* gene expression was not down regulated by OM-related cytokines.**

Previous studies conducted in our laboratory have shown that the growth-inhibitory activity of OM in the breast cancer H3922 cells is a unique function of this cytokine. Several OM-related cytokines including IL-6, IL-11, and LIF did not inhibit the cellular proliferation of H3922 cells and other breast cancer cell lines such as MCF-7. We were interested in investigating whether these factors regulate BCSG1 gene expression. H3922 cells were treated with OM, IL-6, IL-11, and LIF for 24 h at 100 ng/ml concentration for each factor respectively. The result of northern blot analysis show that BCSG1 mRNA expression was specifically regulated by OM, but not by the other cytokines (Figure 6). These data suggest that the down regulation of BCSG1 expression is concurrently associated with the suppression of cell growth.

2. Suppression of EGF-mediated tyrosine phosphorylation by pretreatment of breast cancer cells with oncostatin M

Previously, we have shown that stimulation of H3922 cells with EGF increases cellular proliferation to 3-4-fold higher than that observed in untreated cells. Simultaneous treatment of H3922 cells with OM causes a time- and dose-dependent antagonistic effect on EGF-stimulated

growth. In order to investigate the impact of OM on EGF-mediated signal transduction, we examined EGF-induced tyrosine phosphorylation events in H3922 cells that had been pretreated with OM for different lengths of times. Tyrosine phosphorylated proteins were immunoprecipitated from total cell lysates derived from H3922 cells treated under various conditions. Subsequent western blot analysis demonstrated that EGF stimulation transiently induces tyrosine phosphorylation of several cellular proteins including the EGF receptors (EGFR). Pretreatment of H3922 cells with OM for 6 to 48 hours prior to EGF stimulation did not affect tyrosine phosphorylation. However, 72 hours pretreatment of cells with OM severely diminished the tyrosine phosphorylation events induced by EGF (Figure 7). We also observed that the maximal inhibitory effect of OM on H3922 cell proliferation occurs after three days treatment. We are currently investigating the mechanism by which OM affects the cellular tyrosine phosphorylation event and the correlation between cell proliferation and tyrosine phosphorylation.

3. Detections of endogenous expressed OM in tumor tissue section.

One characteristic of the host response to tumor growth is the infiltration of tumors by macrophages and T lymphocytes. Production of tumor-inhibitory cytokines in a timely and locally released fashion may represent an important function of the host defense system to suppress tumor progression. From this prospective view, the inhibition of breast tumor growth by OM, a cytokine predominantly produced by activated T cells and macrophages may represent the tumor-host interaction. To examine this hypothesis, we have initiated a study to examine the OM expression in breast tumors by inflammatory cells. By utilizing anti-OM monoclonal antibodies, we examined OM expression in tissue sections derived from breast cancer and ovarian cancers. The preliminary results showed infiltrating macrophages and neutrophils in breast tumors were positive with anti-OM mAbs. (Figure 8). This immunostaining signals were blocked with addition of recombinant human OM in the incubation medium. Interestingly, high levels of anti-OM immunoreactivity were detected in mucinous epithelial cells in ovarian tumors (Figure 9). The expression of OM are associated with the low malignant potential of this type of ovarian tumor. Whether the high level expression of OM in ovarian tumors plays a functional role in mucinous epithelial cells transformation need to be further investigated. We currently in the process to conduct in situ hybridization to examine the mRNA expression of OM in breast and ovarian tumor sections.

D. CONCLUSION

The results described in this report demonstrate that

- 1) BCSG1 gene expression is associated with breast cancer development and progression.
- 2) BCSG1 is transcriptional suppressed by OM in a breast cancer cell line which is growth-inhibited by OM. That suggests BCSG1 expression may be involved in the process of OM-mediated growth inhibition.
- 3) In OM treated H3922 cells, EGF no longer be able to induce the EGF receptor intrinsic tyrosine kinase activity. This may account for at least in part the mechanism by which OM antagonizes the EGF mitogenic activity.

4) The expression of OM by inflammatory cells that were infiltrating breast tumors suggest that OM may plays a functional role in vivo as a part of body defence system to inhibit tumor growth and progression.

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Figure 1

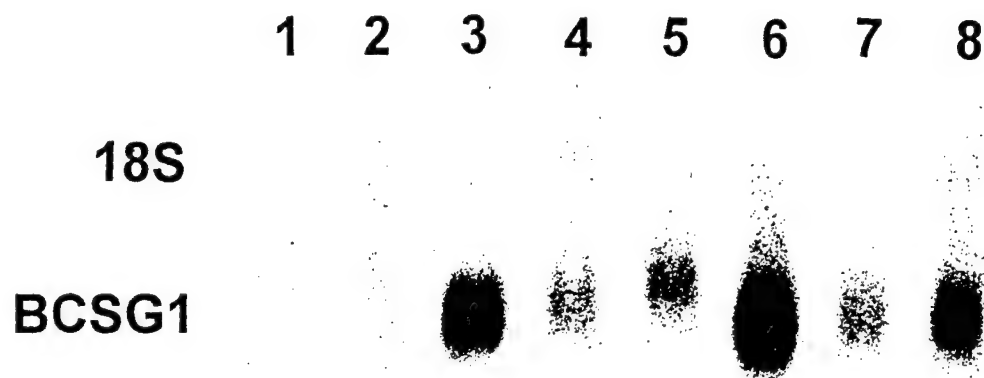


Figure 2

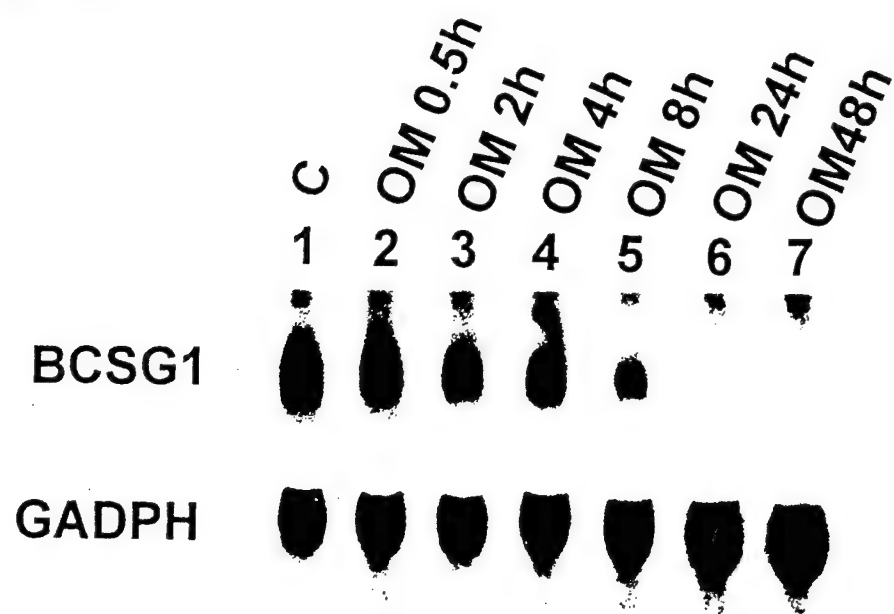


Figure 3A

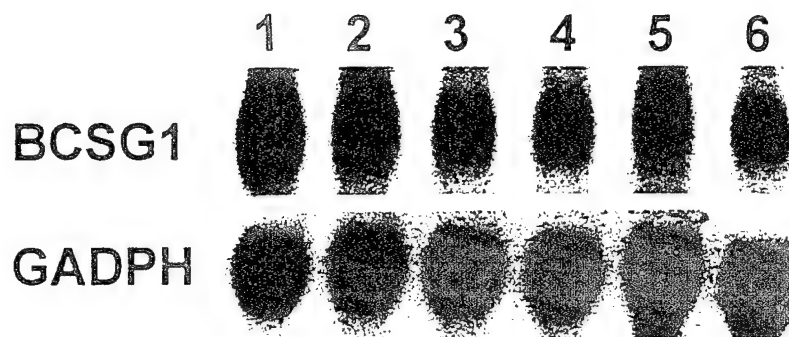


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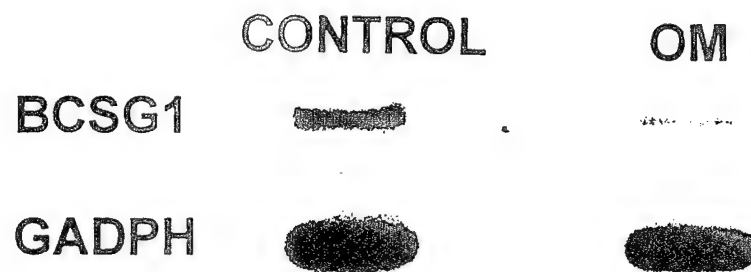


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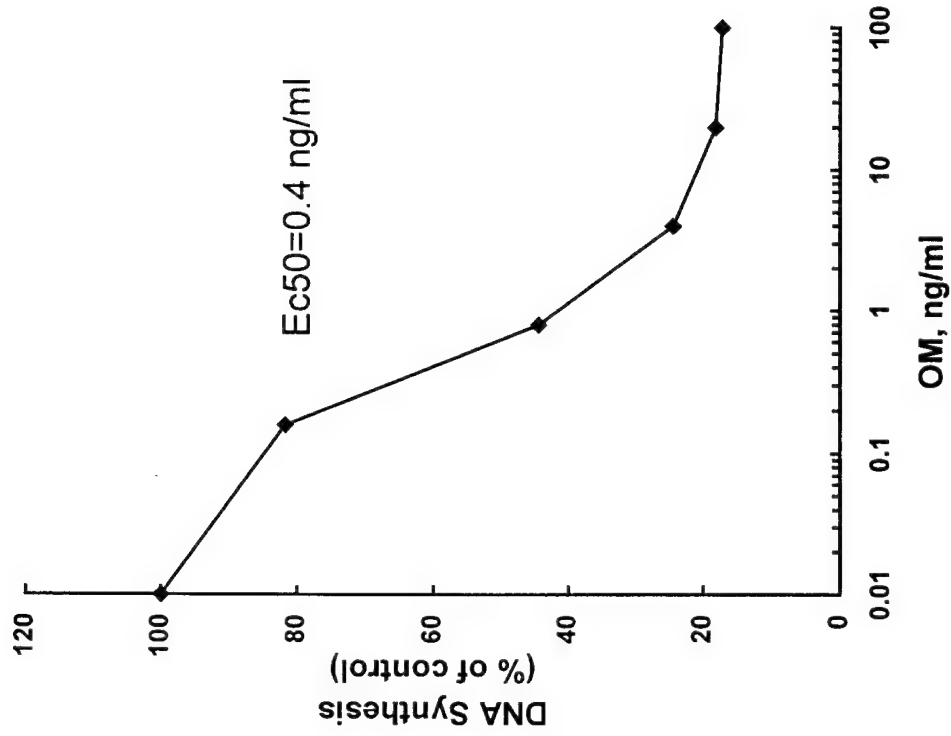


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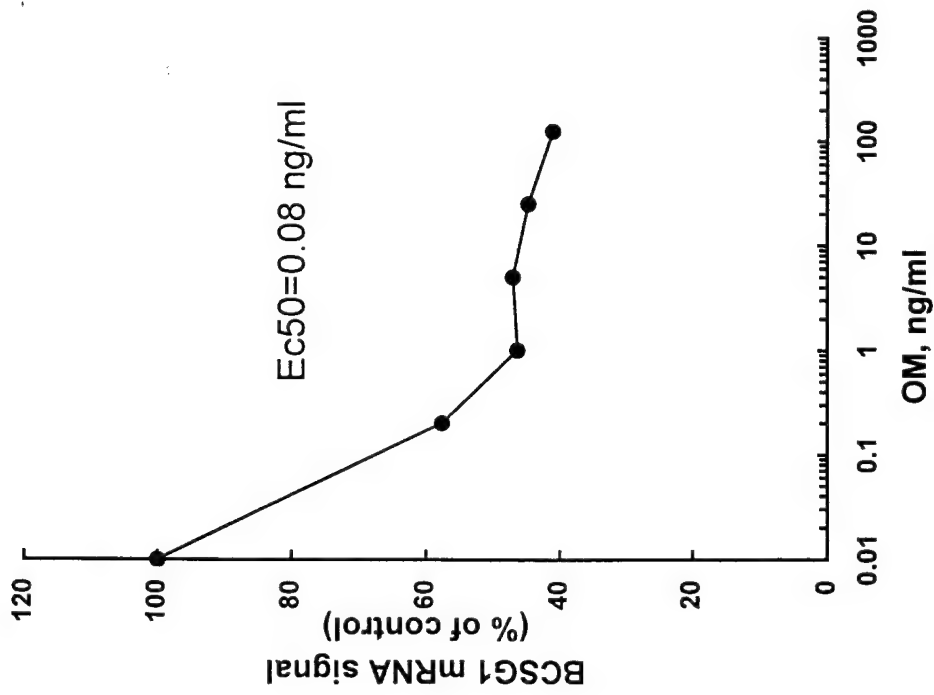


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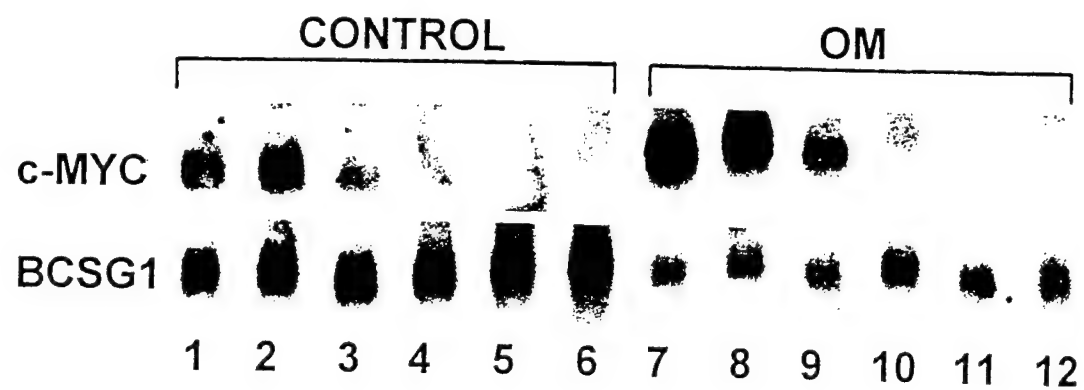


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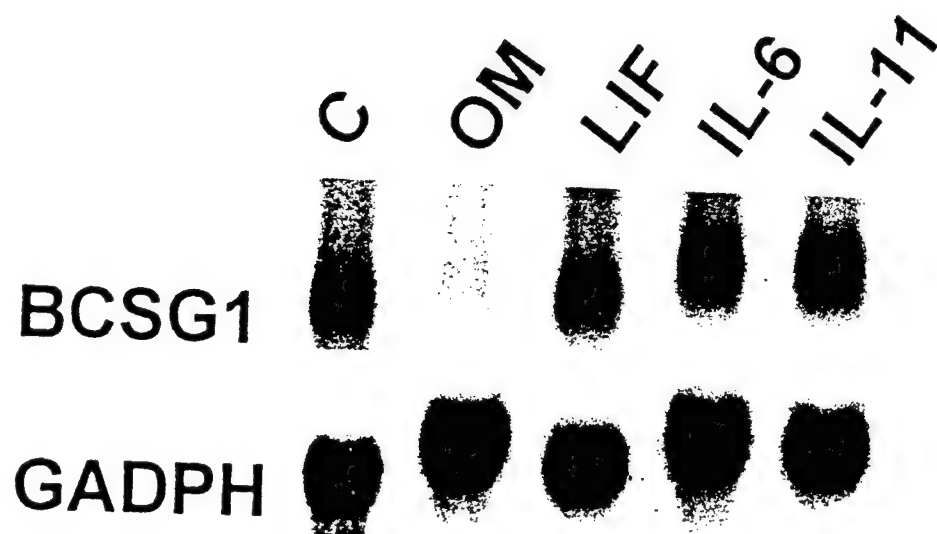


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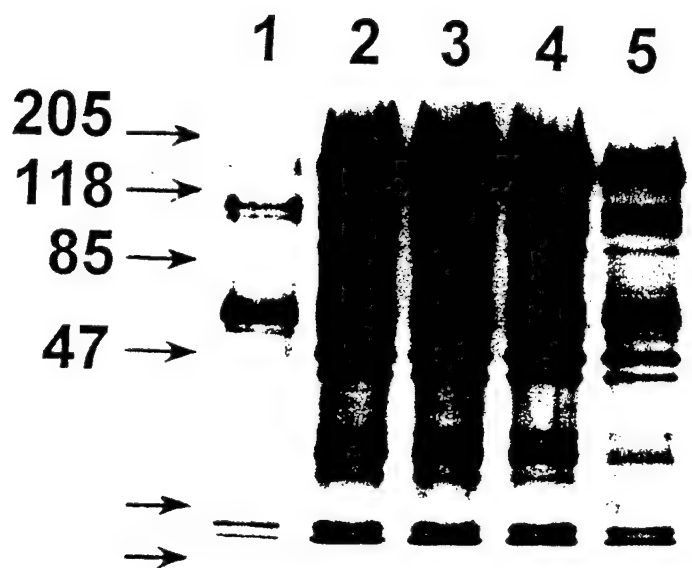
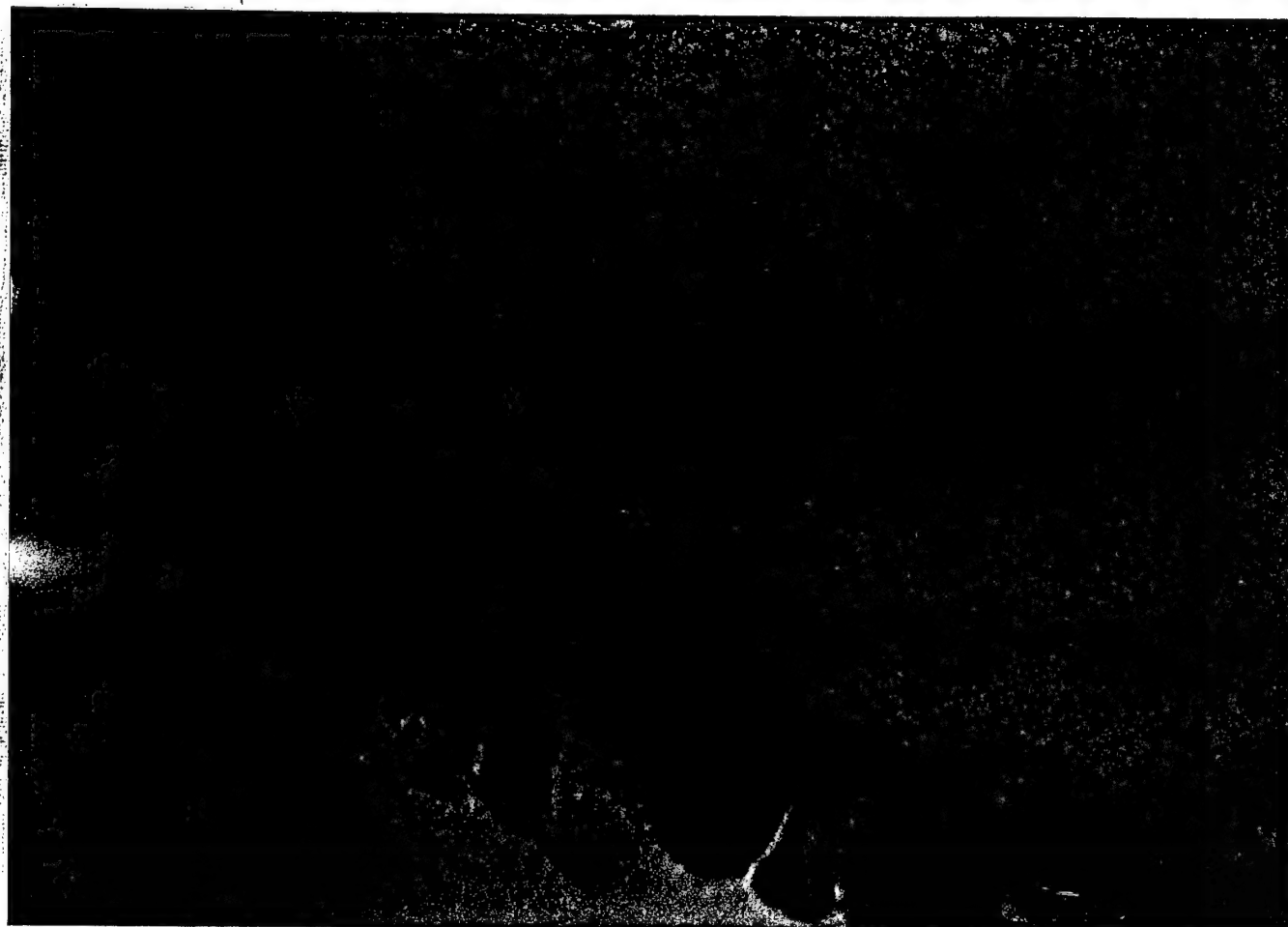


Figure 8



• • • Figure 9



G. FIGURE LEGENDS

Figure 1. Northern blot analysis of *BCSG1* expression in human breast cancer cell lines.

Total RNA was isolated and analyzed by northern blot. Lane 1, H3396 (derived from pleural effusion); Lane 2, MCF-7 (derived from pleural effusion); Lane 3, SKBR-3 (pleural effusion); lane 4, MDAMB-231 (pleural effusion); Lane 5, H3914 (infiltrating ductal carcinoma); lane 6, H3922 (infiltrating ductal carcinoma); Lane 7, ZR-75-1 (infiltrating ductal carcinoma); Lane 8, T47D (infiltrating ductal carcinoma).

Figure 2. Time-dependent suppression of *BCSG1* mRNA expression by OM.

Total RNA (20 µg/lane) was isolated from H3922 cells that were cultured in 2% FBS IMEM and treated with OM at a dose of 20 ng/ml for the indicated lengths of time. RNA samples were blotted onto a nylon membrane and hybridized to a ³²P-labeled 0.55 Kb *BCSG1* cDNA probe as described in "Materials and Methods". The blot was rehybridized under the same conditions with a ³²P-labeled human *GAPDH* probe. Radioactive signals were detected by autoradiography and quantified by densitometry.

Figure 3. OM-concentration dependent effects on *BCSG1* mRNA expression and on cellular proliferation.

A. Total RNA (20 µg/lane) was isolated from H3922 cells that were untreated (lane 1), 0.2 ng/ml OM-treated (lane 2), 1.0 ng/ml OM-treated (lane 3), 5.0 ng/ml OM-treated (lane 4), 25 ng/ml OM-treated (lane 5), or 125.0 ng/ml OM-treated (lane 6). All OM treatments were for 6 h. RNA samples were analyzed as described in figure 1. B. The relative levels of *BCSG1* mRNA normalized to *GAPDH* mRNA on the autoradiograph shown in panel A were quantitated by scanning densitometry. The figure shown is representative of two separate experiments. C. H3922 cells (3000 cells/well) were incubated for 72 hours in IMDM containing 2% FBS with the indicated amount of purified human recombinant OM. Cells were pulsed with [³H]thymidine for an additional 4 hours. The amount of radioactivity incorporated into the cells was determined by scintillation assay and the data were expressed as percentages of that observed in the untreated controls.

Figure 4. Nuclear runon analysis of *BCSG1* transcription. Two slots were blotted onto each of two nylon membrane strips. One slot received 3 µg of the 0.3 kb fragment of the *BCSG1* cDNA which is the 3' end of the cDNA. This fragment was generated by cutting the *BCSG1* cDNA with the restriction endonuclease BstX1. The second slot was loaded with 5 µg of the *GAPDH* plasmid. One nylon strip was hybridized to a ³²P-radiolabeled nuclear runon reaction prepared from 16-h OM-treated H3922 cells. The second was hybridized to a labeled nuclear runon reaction prepared from control cells. Equal amount of radioactivity was used in each hybridization. Radioactive signals were detected by autoradiography and quantified by densitometric analysis. Isolation of nuclei, preparation of nuclear runon reactions, hybridizations and washes were all as described in "Materials and Methods".

Figure 5. OM did not change the *BCSG1* mRNA stability. Cells were either treated with OM at the concentration of 50 ng/ml for 6 h (lane 7-12), or treated with OM dilution buffer, 1 mg/ml

BSA in PBS, for the same length of time (lane 1-6), then actinomycin D at a concentration of 5 µg/ml was added to cells for different lengths of time. At the end of each time point, total RNA was harvested and analyzed for *BCSG1* mRNA and *c-Myc* mRNA expressions as described in Figure 1. The length of actinomycin D treatment: lanes 1 and 7, 0 h; lanes 2 and 8, 0.5 h; lanes 3 and 9, 1 h; lanes 4 and 10, 2 h; lanes 5 and 11, 3 h; lanes 6 and 12, 4 h.

Figure 6. Comparison of effects of OM related cytokines on *BCSG1* gene transcription. H3922 cells were treated for 24 h with each factors at 100 ng/ml concentration respectively. Total RNA was subsequently isolated for northern blot analysis of *BCSG1* mRNA levels.

Figure 7. Oncostatin M has an antagonistic effect on EGF-mediated tyrosine phosphorylation of signaling proteins in H3922 cells. Tyrosine phosphorylated proteins immunoprecipitated from various H3922 cell extracts were detected on a western blot from an SDS-PAGE gel by enhanced chemiluminescence. Lane 1, untreated control cells; Lane 2, OM stimulated ten minutes; Lane 3, EGF stimulated ten minutes; Lane 4, both OM and EGF stimulated ten minutes; Lane 5, OM pretreated 72 hours, followed by EGF stimulation ten minutes. Ten-minute stimulation of H3922 cells with EGF induced tyrosine phosphorylation of many proteins (EGF 10'). Pretreatment of H3922 cells with OM for 72 hours prior to stimulation with EGF (OM72h./EGF10'), reduced the number of detectable tyrosine phosphorylated signals nearly to that observed in the control lane (C). These data demonstrated a clear antagonistic effect of OM on EGF-activated signaling components in H3922 cells.

Figure 8. Immunohistochemical staining with anti-OM mAbs in breast tumor sections. OM staining was detected in neutrophil cells. In breast tumor section, the malignant epithelial cells were negative.

Figure 9. OM positive staining in mucinous epithelial cells in ovarian tumors.

H. PUBLICATIONS (5/1996-4/1997)

1. Liu J, Wallace PM, Forcier K, Hellström I, Vestal RE: Oncostatin M-specific receptor mediates inhibition of breast cancer cell growth, antagonism of growth factors, and down regulation of c-myc protooncogene. *Cell Growth & Differentiation*, June, 1997.
2. Spence M, Vestal RE, and Liu J: Suppression of c-myc proto oncogene by oncostatin M in breast cancer cells. *Cancer Research*, June, 1997..
3. Shi YE, Wang M, Jia T, Liu J, Fuchs A, Rosen C, Liu YE, and Ji H: Identification of breast cancer specific gene, BCSG1, by direct differential cDNA sequencing. *Cancer Research* 57:759-764, 1997.
4. Liu J, Streiff R, Vestal E, and Briggs M: Novel Mechanism of Transcriptional Activation of Hepatic LDL Receptor by Oncostatin M, *J. Lipid. Res* in press.
5. Liu J, Zhang YL, Spence MJ, Wallace PM, and Grass D: Liver LDL receptor mRNA in human ApoB and CETP double transgenic mice is down regulated by high-cholesterol diet and up regulated by cytokine oncostatin M. *Arteriosclerosis and Thrombosis in press*.
6. Liu J, Hadjokas N, Mosley B, Vestal RE: Oncostatin M-specific receptor expression and function in regulating cell proliferation of normal and malignant mammary epithelial cells. Submitted to Cytokines.
7. Liu J, Spence MJ Zhang YL, Jia T., Shi E: Transcriptional suppression of the breast cancer specific gene (*BCSG1*) expression by the cytokine oncostatin M. Submitted to Cancer Research.
8. Spence M, Vestal RE, and Liu J: Oncostatin M suppresses the EGF-induced intrinsic EGF receptor tyrosine phosphorylation activity.

I. AWARD

One of the two recipients for **Young Investigator Award**, International Cytokine Society, October 1996

Request for Immunex Research Materials

This Request must be completed and signed by the Investigator and an authorized representative of the Institution with which the Investigator is affiliated. The fully signed form must be returned by mail (**do not fax**) to Kathleen S. Picha, Immunex Corporation; 51 University Street, Seattle, WA 98101. Requests will be granted based on scientific merit, mutual interest and reagent availability.

Name of Investigator: Jingwen Liu, Ph.D.

Title or Function: Chief, Molecular pharmacology Research Laboratory

Name of Institution: Veterans Affairs Medical Center

Office Address: Research Service, VA Medical Center
500 West Fort Street, Boise, ID 83702

Telephone Number: (208) 422-1000 ext. 7682 Facsimile Number: (208) 422-1155

E-mail: jingliu@micron.net

Relevant Immunex contact(s): Bruce Mosley

Materials Requested (please specify reagent, species, and quantity or amount):
Human ~~recombinant~~ Oncostatin M receptor beta subunit cDNA
in a mammalian expression vector (OSMR-beta)
in microgram quantity.

Address to which Materials are to be shipped: VA Medical Center
500 West Fort St. Boise, ID 83702

Federal Express Account Number or Credit Card Number and Expiration Date (to cover shipping costs only):

Federal Express Account #: 1424-9489-2

Address at which Materials will be stored: Molecular pharmacology Research Laboratory, VA Medical Center
500 W. Fort St. Boise, ID 83702

Please describe proposed use of requested materials in one or two paragraphs:

We have been collaborating with Bruce Mosley to investigate the Oncostatin M receptor (OSMR) mediated growth inhibition of breast cancer cells. Several Breast cancer cell lines do not express OSMR and lack the response to OSM-mediated growth regression. Therefore, we would like to transfect OSMR-beta cDNA into these cells and to test their response to OSM.

Keywords (please mark all that apply)

- | | | | | |
|---|---|--|---|---|
| <input type="checkbox"/> AIDS models | <input type="checkbox"/> Dendritic Cell Biology | <input type="checkbox"/> Immunodeficiency | <input type="checkbox"/> Neurobiology | <input type="checkbox"/> Tumor Immunology |
| <input type="checkbox"/> Adjuvants | <input type="checkbox"/> Developmental Biology | <input type="checkbox"/> Infectious Disease | <input type="checkbox"/> Pharmacology | <input type="checkbox"/> TURF |
| <input type="checkbox"/> Antigen Presentation | <input type="checkbox"/> ECCAT | <input type="checkbox"/> Inflammation | <input type="checkbox"/> Reproductive Biology | <input type="checkbox"/> Urinary System Biology |
| <input type="checkbox"/> Autoimmunity | <input checked="" type="checkbox"/> Endocrinology | <input type="checkbox"/> Joint/Connective Tissue Biology | <input type="checkbox"/> Respiratory Biology | <input type="checkbox"/> Vascular Biology |
| <input type="checkbox"/> B cell Biology | <input type="checkbox"/> Gastrointestinal Biology | <input type="checkbox"/> Mast Cell Biology | <input checked="" type="checkbox"/> Signal Transduction | <input type="checkbox"/> Virology |
| <input type="checkbox"/> Bone Biology | <input type="checkbox"/> Gene Therapy | <input type="checkbox"/> Metabolism | <input type="checkbox"/> Skin Biology | <input type="checkbox"/> Other (please specify) |
| <input type="checkbox"/> Cardiac Biology | <input type="checkbox"/> Genetic Disorders | <input type="checkbox"/> Muscle Biology | <input type="checkbox"/> T cell Biology | |
| <input type="checkbox"/> Cell Adhesion | <input type="checkbox"/> HIV/SIV | <input type="checkbox"/> NK cell Biology | <input type="checkbox"/> Tissue Repair | |
| <input type="checkbox"/> Cell Death | <input type="checkbox"/> Hematopoiesis Biology | <input type="checkbox"/> Neoplasia | <input type="checkbox"/> Transplantation | |
| <input type="checkbox"/> Cytokine Induction | <input type="checkbox"/> Hypersensitivity | | <input type="checkbox"/> Tumor Drug Resistance | |

Questions concerning this Agreement should be directed to Immunex Extramural Research (206) 389-4026.

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3. Delivery of Materials. Immunex shall deliver the requested Materials to the Investigator within a reasonable period of time after this Agreement is fully-executed by the parties. Immunex shall determine the quantities to be transferred to the Investigator.

4. Use of Materials. As of the date this Agreement is executed by Immunex, Immunex grants the Investigator a non-exclusive license to use the Materials for the Proposed Use for academic research purposes only and not for any commercial use. The Investigator shall not use the Materials in humans or in contact with any cells or other materials to be infused into humans. Use of the Materials to prepare somatic cell therapy products or gene therapy products is specifically prohibited. The Investigator shall use the Materials in compliance with all applicable federal, state and local laws and regulations. The Investigator shall not transfer the Materials to any person who is not under the immediate and direct supervision of the Investigator, nor use the Materials in research that is subject to consulting or licensing obligations to another corporation or a government agency, other than the NIH, unless prior written permission is obtained from Immunex.

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The signatures of the authorized officers of each party are required below to make the Agreement effective.

IMMUNEX CORPORATION

Michael B. Widmer

Michael B. Widmer, Ph.D.
Vice President, Director of Biological Sciences

April 4, 1997

Date

The provisions of the foregoing are agreed to and accepted by:

Jingwen Liu, ph.D.

Investigator

4/7/97

Date

VA Medical Center
Boise, ID

Name of Institution

Wayne J. R.

Authorized Representative of Institution

Medical Center Director

Title

4-7-97

Date

Rev. 1/97